

SEQUENCE LISTING

<110> Liaw, Gin
 Pedersen, Sven
 Hendriksen, Sven

<120> A Method of Producing Saccharide
 Preparations

<130> 5318.200-US

<140> 09/198,672
 <141> 1998-11-23

<160> 5

<170> FastSEQ for Windows Version 3.0

<210> 1
 <211> 1605
 <212> DNA
 <213> Aspergillus Niger

<220>
 <221> sig_peptide
 <222> (1)...(72)

<221> mat_peptide
 <222> (73)...(1602)

<221> CDS
 <222> (1)...(1602)

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-20 -15 -10	

ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser	96
-5 1 5	

aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala	144
10 15 20	

gac ggt gct tgg gtg tcg ggc gcg gac tct ggc att gtc gtt gct agt Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser	192
25 30 35 40	

ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser	240
45 50 55	

ggt ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr	288
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60	65	70	
agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val	75	80	336
cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu	90	95	384
ggg gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp	105	110	432
gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile	125	130	480
ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr	140	145	528
gac att gtt tgg ccc ctc gtt agg aac gac ctg tcg tat gtg gct caa Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln	155	160	576
tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tcg Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser	170	175	624
tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser	185	190	672
gcc ttc gcg acg gcc gtc ggc tcg tcc tgc tcc tgg tgt gat tct cag Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln	205	210	720
gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe	220	225	768
att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr	235	240	816
ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp	250	255	864
tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu	265	270	912
gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser	285	290	960
			295

gac agc gag gct gtt gcg gtg ggt cgg tac cct gag gac acg tac tac Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr 300 305 310	1008
aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Glu Gln Leu 315 320 325	1056
tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr 330 335 340	1104
gat gtg tcg ctg gac ttc ttc aag gca ctg tac agc gat gct gct act Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr 345 350 355 360	1152
ggc acc tac tct tcg tcc agt tcg act tat agt agc att gta gat gcc Gly Thr Tyr Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala 365 370 375	1200
gtg aag act ttc gcc gat ggc ttc gtc tct att gtg gaa act cac gcc Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala 380 385 390	1248
gca agc aac ggc tcc atg tcc gag caa tac gac aag tct gat ggc gag Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu 395 400 405	1296
cag ctt tcc gct cgc gac ctg acc tgg tct tat gct gct ctg ctg acc Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr 410 415 420	1344
gcc aac aac cgt aac tcc gtc gtg cct gct tct tgg ggc gag acc Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr 425 430 435 440	1392
tct gcc agc agc gtg ccc ggc acc tgt gcg gcc aca tct gcc att ggt Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly 445 450 455	1440
acc tac agc agt gtg act gtc acc tcg tgg ccg agt atc gtg gct act Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr 460 465 470	1488
ggc ggc acc act acg acg gct acc ccc act gga tcc ggc agc gtg acc Gly Gly Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr 475 480 485	1536
tcg acc agc aag acc acc gcg act gct agc aag acc agc acc acg acc Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr 490 495 500	1584
cgc tct ggt atg tca ctg tga Arg Ser Gly Met Ser Leu 505 510	1605

<210> 2
<211> 534
<212> PRT
<213> Aspergillus Niger

<220>
<221> SIGNAL
<222> (1)...(24)

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-5 1 5
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
10 15 20
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
25 30 35 40
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
45 50 55
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
60 65 70
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
75 80 85
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
90 95 100
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
105 110 115 120
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
125 130 135
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
140 145 150
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
155 160 165
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
170 175 180
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
185 190 195 200
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
205 210 215
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
220 225 230
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
235 240 245
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
250 255 260
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
265 270 275 280
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
285 290 295
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
300 305 310
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
315 320 325
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
330 335 340

Asp	Val	Ser	Leu	Asp	Phe	Phe	Lys	Ala	Leu	Tyr	Ser	Asp	Ala	Ala	Thr
345				350						355					360
Gly	Thr	Tyr	Ser	Ser	Ser	Ser	Ser	Thr	Tyr	Ser	Ser	Ile	Val	Asp	Ala
				365					370					375	
Val	Lys	Thr	Phe	Ala	Asp	Gly	Phe	Val	Ser	Ile	Val	Glu	Thr	His	Ala
				380				385				390			
Ala	Ser	Asn	Gly	Ser	Met	Ser	Glu	Gln	Tyr	Asp	Lys	Ser	Asp	Gly	Glu
				395			400			405					
Gln	Leu	Ser	Ala	Arg	Asp	Leu	Thr	Trp	Ser	Tyr	Ala	Ala	Leu	Leu	Thr
				410			415			420					
Ala	Asn	Asn	Arg	Arg	Asn	Ser	Val	Val	Pro	Ala	Ser	Trp	Gly	Glu	Thr
				425			430			435			440		
Ser	Ala	Ser	Ser	Val	Pro	Gly	Thr	Cys	Ala	Ala	Thr	Ser	Ala	Ile	Gly
				445				450			455				
Thr	Tyr	Ser	Ser	Val	Thr	Val	Thr	Ser	Trp	Pro	Ser	Ile	Val	Ala	Thr
				460			465			470					
Gly	Gly	Thr	Thr	Thr	Thr	Ala	Thr	Pro	Thr	Gly	Ser	Gly	Ser	Val	Thr
				475			480			485					
Ser	Thr	Ser	Lys	Thr	Thr	Ala	Thr	Ala	Ser	Lys	Thr	Ser	Thr	Thr	Thr
				490			495			500					
Arg	Ser	Gly	Met	Ser	Leu										
				505			510								

<210> 3
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<212> DNA
<213> Artificial Sequence

<220>
<223> primers

<400> 3

gaatgacttg	gttgacgcgt	caccagtcac	30
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<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> primers

<400> 4

ggggatcatg	ataggactag	ccatatataat	gaagggcata	taccacgcct	tggacctgcg	60
ttatagcc						68

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primers

<400> 5

cctacactgg	tccttgggga	cggc	24
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